Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	682	(untranslated adj1 region) same (DNA) same (remov$)	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 13:40
L2	740	(untranslated adj1 region or UTR) same (DNA) same (remov$)	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 13:40
L3	158	l2 and exonuclease	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 13:40
L4	123	l3 and (nuclease or mung)	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 13:53
L5	417	(site-directed adj1 mutagenesis) same (exonuclease)	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 13:54
L6	191	l5 and (nuclease or Mung adj1 bean)	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 13:59
L7	8388	(exonuclease) and (nuclease or Mung adj1 bean)	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 13:59
L8	4742	l7 and mutagenesis	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 13:59
L9	2863	l8 and removal	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 13:59
L10	276	l9 and UTR	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 14:27
L11	20	hammond-philip-w.in.	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 14:36
L12	4133	hammond.in.	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 14:36
L13	11	l12 and UTR	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 14:37

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	6689	(cDNA) same (blunt or cohesive)	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 15:42
L2	2	l1 and exonulcease	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 15:43
L3	8205	(cDNA) same (mutagenesis)	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 15:43
L4	1227	l3 and exonuclease	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 15:44
L5	210	l4 and (mung adj1 bean adj1 nuclease)	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 15:52
L6	420	(exonuclease adj1 III) same (mung adj1 bean adj1 nuclease)	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 15:53
L7	340	l6 and cDNA	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 16:05
L8	284	(deletion adj1 mutations)same cDNA	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 16:23
L9	2	"6489145".pn.	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 16:27
L10	2	"6337186".pn.	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 16:35
L11	1600	carlsson.in.	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 16:36
L12	73390	l11 recombination	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 16:36
L13	9	l11 and recombination	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 16:38
L14	2	invitro adj1 recombination	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 16:39
L15	302	in adj1 vitro adj1 recombination	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 16:40

L16	150	l15 and exonuclease	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 16:40
L17	24	l16 and mung	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 16:40

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                   alerts (SDIs) affected
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                   alerts (SDIs) affected
 NEWS  12 DEC 17   CERAB reloaded; updating to resume; current-awareness
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 NEWS  13 DEC 17   THREE NEW FIELDS ADDED TO IFIPAT/IFIUDB/IFICDB
 NEWS  14 DEC 30   EPFULL: New patent full text database to be available on STN
 NEWS  15 DEC 30   CAPLUS - PATENT COVERAGE EXPANDED
 NEWS  16 JAN 03   No connect-hour charges in EPFULL during January and
                   February 2005
 NEWS  17 FEB 25   CA/CAPLUS - Russian Agency for Patents and Trademarks
                   (ROSPATENT) added to list of core patent offices covered
 NEWS  18 FEB 10   STN Patent Forums to be held in March 2005
 NEWS  19 FEB 16   STN User Update to be held in conjunction with the 229th ACS
                   National Meeting on March 13, 2005
 NEWS  20 FEB 28   PATDPAFULL - New display fields provide for legal status
                   data from INPADOC
 NEWS  21 FEB 28   BABS - Current-awareness alerts (SDIs) available
 NEWS  22 FEB 28   MEDLINE/LMEDLINE reloaded
 NEWS  23 MAR 02   GBFULL: New full-text patent database on STN
 NEWS  24 MAR 03   REGISTRY/ZREGISTRY - Sequence annotations enhanced
 NEWS  25 MAR 03   MEDLINE file segment of TOXCENTER reloaded

 NEWS EXPRESS  JANUARY 10 CURRENT WINDOWS VERSION IS V7.01a, CURRENT
               MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
               AND CURRENT DISCOVER FILE IS DATED 10 JANUARY 2005

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COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                         ENTRY    SESSION
FULL ESTIMATED COST                                       0.06       0.27

FILE 'HOME' ENTERED AT 14:46:38 ON 08 MAR 2005

=> FIL BIOSIS, EMBASE, MEDLINE, LIFESCI, CAPLUS
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
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=> s (UTR or untranslated (1a) region) (S) (ORF or open (1a) reading (1a) frame or cDNA)
L1       13822 (UTR OR UNTRANSLATED (1A) REGION) (S) (ORF OR OPEN (1A) READING
               (1A) FRAME OR CDNA)

=> s l1 and (diges?)
L2         543 L1 AND (DIGES?)

=> s l2 and exonuclease
L3           1 L2 AND EXONUCLEASE

=> d l3
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CS Department of Molecular Biology, Okayama University Medical School, Japan.
SO Biochimica et biophysica acta, (1992 Jul 15) 1131 (3) 287-99.
Journal code: 0217513. ISSN: 0006-3002.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-D13370; GENBANK-D90373; GENBANK-M80475; GENBANK-M80476; GENBANK-M80530; GENBANK-M80531; GENBANK-M80532; GENBANK-M80533; GENBANK-M91429; GENBANK-M91430
EM 199208
ED Entered STN: 19920904
Last Updated on STN: 20000303
Entered Medline: 19920820

L5 ANSWER 4 OF 5 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2000:133874 CAPLUS
DN 132:190497
TI Methods of producing mRNA-protein conjugates and optimizing their formation by removing mRNA 3'-untranslated regions
IN Hammond, Philip W.; Lipovsek, Dasa
PA Phylos, Inc., USA
SO PCT Int. Appl., 52 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000009737	A1	20000224	WO 1999-US18603	19990816
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	CA 2334946	AA	20000224	CA 1999-2334946	19990816
	AU 9954883	A1	20000306	AU 1999-54883	19990816
	EP 1105516	A1	20010613	EP 1999-941179	19990816
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	US 6312927	B1	20011106	US 1999-374962	19990816
	JP 2002522091	T2	20020723	JP 2000-565171	19990816
	US 2002160377	A1	20021031	US 2001-910518	20010720
	US 2004086980	A1	20040506	US 2003-646985	20030821
PRAI	US 1998-96818P	P	19980817		
	US 1999-374962	A3	19990816		
	WO 1999-US18603	W	19990816		
	US 2001-910518	B1	20010720		

RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 5 OF 5 CAPLUS COPYRIGHT 2005 ACS on STN
AN 1993:423523 CAPLUS
DN 119:23523
TI cDNA cloning, sequencing, expression and possible domain structure of human APEX **nuclease** homologous to Escherichia coli **exonuclease** III
AU Seki, Shuji; Hatsushika, Masao; Watanabe, Sekiko; Akiyama, Kosuke; Nagao, Kazutaka; Tsutsui, Ken
CS Okayama Univ. Med. Sch., Okayama, Japan
SO Biochimica et Biophysica Acta (1992), 1131(3), 287-99
CODEN: BBACAQ; ISSN: 0006-3002
DT Journal
LA English

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=> file Medline
COST IN U.S. DOLLARS                                    SINCE FILE      TOTAL
                                                           ENTRY    SESSION
FULL ESTIMATED COST                                        38.70      39.18

FILE 'MEDLINE' ENTERED AT 14:52:29 ON 08 MAR 2005

 FILE LAST UPDATED: 5 MAR 2005 (20050305/UP).  FILE COVERS 1950 TO DATE.

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    http://www.nlm.nih.gov/mesh/
    http://www.nlm.nih.gov/pubs/techbull/nd04/nd04_mesh.html

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 MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the
 MeSH 2005 vocabulary.

 This file contains CAS Registry Numbers for easy and accurate
 substance identification.

=> E HAMMOND P W/AU 25
E1            6     HAMMOND P S/AU
E2            9     HAMMOND P V/AU
E3           10 --> HAMMOND P W/AU
E4            2     HAMMOND PAMELA I/AU
E5            1     HAMMOND PAUL A/AU
E6            5     HAMMOND PAULA T/AU
E7            1     HAMMOND PAULINE/AU
E8            3     HAMMOND PETER/AU
E9            6     HAMMOND PHIL/AU
E10           2     HAMMOND PHILIP W/AU
E11           1     HAMMOND PHILLIP S/AU
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E13          24     HAMMOND R A/AU
E14           4     HAMMOND R B/AU
E15          19     HAMMOND R C/AU
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E22           7     HAMMOND R K/AU
E23          63     HAMMOND R L/AU
E24           6     HAMMOND R M/AU
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=> S (E3) AND 1990<=PY<=1998
            10 "HAMMOND P W"/AU
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L6            5 ("HAMMOND P W"/AU) AND 1990<=PY<=1998

=> DIS L6 1 IBIB ABS

L6   ANSWER 1 OF 5     MEDLINE on STN
ACCESSION NUMBER:   1998215641     MEDLINE
DOCUMENT NUMBER:    PubMed ID: 9548747
TITLE:              Euplotes telomerase: evidence for limited base-pairing
                    during primer elongation and dGTP as an effector of
                    translocation.
AUTHOR:             Hammond P W; Cech T R
```

CORPORATE SOURCE: Department of Chemistry and Biochemistry, Howard Hughes Medical Institute, University of Colorado, Boulder, Colorado 80309-0215, USA.
CONTRACT NUMBER: GM28039 (NIGMS)
SOURCE: Biochemistry, **(1998 Apr 14)** 37 (15) 5162-72.
Journal code: 0370623. ISSN: 0006-2960.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199805
ENTRY DATE: Entered STN: 19980520
Last Updated on STN: 19980520
Entered Medline: 19980514

AB The telomeric sequence repeats at the ends of eukaryotic chromosomes are maintained by the ribonucleoprotein enzyme telomerase. Telomeric DNA primers are bound by telomerase both at the active site, which includes base-pairing with the RNA template, and at a second anchor site. The stabilities of Euplotes aediculatus primer-telomerase complexes were determined by measuring their dissociation rates (koff), using an assay involving photo-cross-linking at the anchor site. The primer length was varied, and mismatched substitutions were introduced in a systematic manner. We observed that koff does not scale with primer length as expected for accumulated primer-template base-pairing. This suggests that telomerase maintains a more-or-less constant number of base pairs, similar to the transcription bubble maintained by RNA polymerase. An upper limit was estimated by comparing the experimental koff for the primer-telomerase complex to that of a model DNA-RNA duplex. All the binding energy could be attributed to 10 or 11 base pairs; alternatively, there could be <10 base pairs, with the remaining energy contributed by other parts of telomerase. Most primers exhibited biphasic dissociation kinetics, with variations in both the amount in each phase and the rate for each phase. Since the cross-links monitored in the dissociation assay were all formed with the 5' region of the primer, the two phases may arise from different base-pairing registers with the RNA template, possibly representing pre- and post-translocation complexes. A shift from slow phase to fast phase dissociation was observed in the presence of dGTP, which may implicate dGTP as a positive effector of translocation.

=> DIS L6 2- IBIB ABS
YOU HAVE REQUESTED DATA FROM 4 ANSWERS - CONTINUE? Y/(N):Y

L6 ANSWER 2 OF 5 MEDLINE on STN
ACCESSION NUMBER: 97426515 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9278493
TITLE: dGTP-dependent processivity and possible template switching of euplotes telomerase.
AUTHOR: **Hammond P W**; Cech T R
CORPORATE SOURCE: Department of Chemistry and Biochemistry, Howard Hughes Medical Institute, University of Colorado, Boulder, CO 80309-0215, USA.
CONTRACT NUMBER: GM28039 (NIGMS)
SOURCE: Nucleic acids research, **(1997 Sep 15)** 25 (18) 3698-704.
Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199710
ENTRY DATE: Entered STN: 19971105
Last Updated on STN: 19971105
Entered Medline: 19971017

AB We have measured the processivity of telomeric DNA extension by Euplotes aediculatus telomerase at various concentrations of the nucleotide substrates dGTP and dTTP. The maximum processivity (approximately 3 repeats) was observed at approximately 100 microM of each dNTP.

Processivity decreased as the dNTP concentrations were reduced and, surprisingly, as the concentration of dGTP was increased. Also, the characteristic banding pattern generated by telomerase extension of DNA primers shifted in response to changes in dGTP concentration. One pattern with 8 nt periodicity was predominant at dGTP concentrations </=16 microM, while at >/= 250 microM an 8 nt repeat pattern out-of-phase with the first was observed; at intermediate concentrations the two patterns coexisted. We propose that two different segments of the RNA subunit can serve as the template for repeat synthesis; nt 42-49 at low dGTP concentrations and nt 36-43 at high dGTP concentrations. An alternative model for the low dGTP pattern involves an internal pause site but no pause at the end of the template and is, therefore, considered less likely. Because the effects of dGTP on processivity and banding pattern appear to be distinct from nucleotide binding in the polymerase active site, we propose a second dGTP binding site involved in template selection and processivity.

L6 ANSWER 3 OF 5 MEDLINE on STN
ACCESSION NUMBER: 97169225 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9016672
TITLE: Detection of all single-base mismatches in solution by chemiluminescence.
AUTHOR: Nelson N C; **Hammond P W**; Matsuda E; Goud A A; Becker M M
CORPORATE SOURCE: Gen-Probe Incorporated, San Diego, CA 92121, USA.
SOURCE: Nucleic acids research, **(1996 Dec 15)** 24 (24) 4998-5003.
Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; AIDS
ENTRY MONTH: 199703
ENTRY DATE: Entered STN: 19970321
Last Updated on STN: 19970321
Entered Medline: 19970311

AB A rapid in-solution method for the detection of all 12 single-base mismatches is described. The technique is based on the hybridization protection assay (HPA) format that utilizes oligonucleotide probes labeled with a highly chemiluminescent acridinium ester (AE). Hydrolysis by weak base renders AE permanently non-chemiluminescent. When an AE-labeled probe hybridizes to an exactly complementary target, AE is protected from hydrolysis relative to the unhybridized conformation. Single-base mutations in the duplex adjacent to the site of AE attachment disrupt this protection resulting in rapid AE hydrolysis and loss of chemiluminescence. The discrimination effect was seen in both DNA and RNA. Studies of Tm values revealed that this effect is not due to a decrease in the overall stability of the duplex, suggesting the AE is responding to local structural changes in the double helix induced by mismatches. Using this principle all 12 single mismatches were clearly discriminated from the corresponding matched sequences. The assay is homogeneous, simple, sensitive, applicable to both amplified and non-amplified targets, and is completed in 30-60 min. An example showing discrimination between wild-type and mutant sequences corresponding to the reverse transcriptase coding region of HIV-1 is given.

L6 ANSWER 4 OF 5 MEDLINE on STN
ACCESSION NUMBER: 97127386 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8972210
TITLE: The anchor site of telomerase from Euplotes aediculatus revealed by photo-cross-linking to single- and double-stranded DNA primers.
AUTHOR: **Hammond P W**; Lively T N; Cech T R
CORPORATE SOURCE: Howard Hughes Medical Institute, Department of Chemistry and Biochemistry, University of Colorado, Boulder 80309-0215, USA.
CONTRACT NUMBER: GM28039 (NIGMS)
SOURCE: Molecular and cellular biology, **(1997 Jan)** 17 (1) 296-308.

Journal code: 8109087. ISSN: 0270-7306.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199701
ENTRY DATE: Entered STN: 19970219
Last Updated on STN: 19970219
Entered Medline: 19970122

AB Telomerase is a ribonucleoprotein enzyme that adds telomeric sequence repeats to the ends of linear chromosomes. In vitro, telomerase has been observed to add repeats to a DNA oligonucleotide primer in a processive manner, leading to the postulation of a DNA anchor site separate from the catalytic site of the enzyme. We have substituted photoreactive 5-iododeoxypyrimidines into the DNA oligonucleotide primer d(T4G4T4G4T4G2) and, upon irradiation, obtained cross-links with the anchor site of telomerase from Euplotes aediculatus nuclear extract. No cross-linking occurred with a primer having the same 5' end and a nontelomeric 3' end. These cross-links were shown to be between the DNA primer and (i) a protein moiety of approximately 130 kDa and (ii) U51-U52 of the telomerase RNA. The cross-linked primer could be extended by telomerase in the presence of [alpha-32P]dGTP, thus indicating that the 3' end was bound in the enzyme active site. The locations of the cross-links within the single-stranded primers were 20 to 22 nucleotides upstream of the 3' end, providing a measure of the length of DNA required to span the telomerase active and anchor sites. When the single-stranded primers are aligned with the G-rich strand of a Euplotes telomere, the cross-linked nucleotides correspond to the duplex region. Consistent with this finding, a cross-link to telomerase was obtained by substitution of 5-iododeoxycytidine into the CA strand of the duplex region of telomere analogs. We conclude that the anchor site in the approximately 130-kDa protein can bind duplex as well as single-stranded DNA, which may be critical for its function at chromosome ends. Quantitation of the processivity with single-stranded DNA primers and double-stranded primers with 3' tails showed that only 60% of the primer remains bound after each repeat addition.

L6 ANSWER 5 OF 5 MEDLINE on STN
ACCESSION NUMBER: 91272856 MEDLINE
DOCUMENT NUMBER: PubMed ID: 2053465
TITLE: Nucleophilic addition to the 9 position of 9-phenylcarboxylate-10-methylacridinium protects against hydrolysis of the ester.
AUTHOR: **Hammond P W**; Wiese W A; Waldrop A A 3rd; Nelson N C; Arnold L J Jr
CORPORATE SOURCE: Gen-Probe Inc., San Diego, CA 92121.
SOURCE: Journal of bioluminescence and chemiluminescence, **(1991 Jan-Mar)** 6 (1) 35-43.
Journal code: 8612490. ISSN: 0884-3996.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199107
ENTRY DATE: Entered STN: 19910811
Last Updated on STN: 19910811
Entered Medline: 19910724

AB The chemiluminescent reaction of an acridinium ester (AE) requires addition of peroxide to the 9 position of the acridinium ring. The addition of a hydroxide ion to the 9 position of an acridinium ester to form the carbinol adduct has also been well documented. We have observed a similar addition of other nucleophiles to the acridinium ring to form an acridan adduct. The adduct formed with bisulphite has been particularly well-characterized for rate of formation, rate of reversion, and reaction equilibrium. The formation of an adduct (other than H2O2) has been demonstrated to decrease significantly the reactivity of the adjacent ester bond to alkaline hydrolysis. The resulting, more stable adduct is very useful when the acridinium ester is used as a label in DNA

probe-based assays. The adduct is highly resistant to hydrolysis under the conditions often desired for DNA probe-based assays (high temperature, elevated pH, extended storage).

```
=> E LIPOVSEK D/AU 25
E1            5     LIPOVOI V V/AU
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E3            4 --> LIPOVSEK D/AU
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E5            6     LIPOVSEK M/AU
E6            1     LIPOVSEK P/AU
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E16           1     LIPOVSKAIA T K/AU
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E22           2     LIPOVSKII I M/AU
E23           1     LIPOVSKII K A/AU
E24           1     LIPOVSKII M A/AU
E25           1     LIPOVSKII S L/AU

=> S (E3)
L7            4 ("LIPOVSEK D"/AU)

=> DIS L7 1- TI
YOU HAVE REQUESTED DATA FROM 4 ANSWERS - CONTINUE? Y/(N):N

=> DIS L7 1- IBIB ABS
YOU HAVE REQUESTED DATA FROM 4 ANSWERS - CONTINUE? Y/(N):Y

L7   ANSWER 1 OF 4     MEDLINE on STN
ACCESSION NUMBER:   1999253497     MEDLINE
DOCUMENT NUMBER:    PubMed ID: 10321580
TITLE:              Hepatitis C virus NS3/4A protease.
AUTHOR:             Kwong A D; Kim J L; Rao G; Lipovsek D; Raybuck S
                    A
CORPORATE SOURCE:   Vertex Pharmaceuticals, Inc., Cambridge, MA 02139, USA..
                    kwong@vpharm.com
SOURCE:             Antiviral research, (1999 Feb) 41 (1) 67-84.  Ref: 100
                    Journal code: 8109699. ISSN: 0166-3542.
PUB. COUNTRY:       Netherlands
DOCUMENT TYPE:      Journal; Article; (JOURNAL ARTICLE)
                    General Review; (REVIEW)
                    (REVIEW, TUTORIAL)
LANGUAGE:           English
FILE SEGMENT:       Priority Journals
ENTRY MONTH:        199907
ENTRY DATE:         Entered STN: 19990816
                    Last Updated on STN: 20000303
                    Entered Medline: 19990730
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AB Despite an urgent medical need, a broadly effective anti-viral therapy for the treatment of infections with hepatitis C viruses (HCVs) has yet to be developed. One of the approaches to anti-HCV drug discovery is the design and development of specific small molecule drugs to inhibit the proteolytic processing of the HCV polyprotein. This proteolytic processing is catalyzed by a chymotrypsin-like serine protease which is located in the N-terminal region of non-structural protein 3 (NS3). This

protease domain forms a tight, non-covalent complex with NS4A, a 54 amino acid activator of NS3 protease. The C-terminal two-thirds of the NS3 protein contain a helicase and a nucleic acid-stimulated nucleoside triphosphatase (NTPase) activities which are probably involved in viral replication. This review will focus on the structure and function of the serine protease activity of NS3/4A and the development of inhibitors of this activity.

L7 ANSWER 2 OF 4 MEDLINE on STN
ACCESSION NUMBER: 1999193949 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10096285
TITLE: Smartbombs and cloaking devices.
COMMENT: Comment on: Nat Biotechnol. 1999 Mar;17(3):265-70. PubMed ID: 10096294
AUTHOR: Wagner R W; **Lipovsek D**
SOURCE: Nature biotechnology, (1999 Mar) 17 (3) 227-8.
Journal code: 9604648. ISSN: 1087-0156.
PUB. COUNTRY: United States
DOCUMENT TYPE: Commentary
News Announcement
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199907
ENTRY DATE: Entered STN: 19990727
Last Updated on STN: 19990727
Entered Medline: 19990712

L7 ANSWER 3 OF 4 MEDLINE on STN
ACCESSION NUMBER: 1999079747 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9864043
TITLE: Hepatitis C virus NS3/4A protease.
AUTHOR: Kwong A D; Kim J L; Rao G; **Lipovsek D**; Raybuck S A
CORPORATE SOURCE: Vertex Pharmaceuticals, Inc., Cambridge, MA 02139, USA.. kwong@vpharm.com
SOURCE: Antiviral research, (1998 Dec) 40 (1-2) 1-18. Ref: 98
Journal code: 8109699. ISSN: 0166-3542.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199903
ENTRY DATE: Entered STN: 19990326
Last Updated on STN: 20000303
Entered Medline: 19990318

AB Despite an urgent medical need, a broadly effective anti-viral therapy for the treatment of infections with hepatitis C viruses (HCVs) has yet to be developed. One of the approaches to anti-HCV drug discovery is the design and development of specific small molecule drugs to inhibit the proteolytic processing of the HCV polyprotein. This proteolytic processing is catalyzed by a chymotrypsin-like serine protease which is located in the N-terminal region of non-structural protein 3 (NS3). This protease domain forms a tight, non-covalent complex with NS4A, a 54 amino acid activator of NS3 protease. The C-terminal two-thirds of the NS3 protein contain a helicase and a nucleic acid-stimulated nucleoside triphosphatase (NTPase) activities which are probably involved in viral replication. This review will focus on the structure and function of the serine protease activity of NS3/4A and the development of inhibitors of this activity.

L7 ANSWER 4 OF 4 MEDLINE on STN
ACCESSION NUMBER: 88006403 MEDLINE
DOCUMENT NUMBER: PubMed ID: 2820881
TITLE: Genes for immunodominant protein antigens are highly homologous in Mycobacterium tuberculosis, Mycobacterium africanum, and the vaccine strain Mycobacterium bovis BCG.

AUTHOR: Lu M C; Lien M H; Becker R E; Heine H C; Buggs A M; **Lipovsek D**; Gupta R; Robbins P W; Grosskinsky C M; Hubbard S C; +
CORPORATE SOURCE: Department of Biology, Massachusetts Institute of Technology, Cambridge 02139.
CONTRACT NUMBER: AI23545 (NIAID)
SOURCE: Infection and immunity, (1987 Oct) 55 (10) 2378-82.
Journal code: 0246127. ISSN: 0019-9567.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198710
ENTRY DATE: Entered STN: 19900305
Last Updated on STN: 19970203
Entered Medline: 19871028
AB The relatedness of immunodominant protein antigens in Mycobacterium tuberculosis, M. africanum, and M. bovis BCG was investigated by comparing the genes that encode major protein antigens in M. tuberculosis with their counterparts in the other two mycobacteria. Genes encoding homologs of M. tuberculosis major protein antigens were isolated from M. africanum and M. bovis BCG by constructing lambda gt11 recombinant DNA expression libraries and screening them with murine monoclonal antibodies and DNA probes. The antibodies were directed against four major protein antigens of M. tuberculosis with molecular masses of 71, 65, 19, and 14 kilodaltons. The isolated M. africanum and M. bovis BCG DNA clones were mapped with restriction endonucleases, and the maps of the mycobacterial genes were confirmed by Southern analysis of mycobacterial genomic DNA. The restriction maps of DNA containing the four genes in M. tuberculosis, M. africanum, and M. bovis BCG are identical, indicating that the immunodominant proteins that they encode are highly homologous in the three mycobacteria. Thus, the immunity against tuberculosis engendered by M. bovis BCG vaccination could be provided, at least in part, by the immune response to these homologous antigens.